

# Exhibit B

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## PROSITE: PDOC00885 (documentation)

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```
{PDOC00885}
{PS01149; PSI_RSU}
{BEGIN}
```

```
*****
* Rsu family of pseudouridine synthase signature *
*****
```

The following bacterial proteins, which seems to belong to a family of pseudouridine synthases (EC [4.2.1.70](#)) [1] have been shown to share regions of similarities:

- Escherichia coli and Haemophilus influenzae 16S pseudouridylate 516 synthase (EC [4.2.1.70](#)) (gene: rsuA). This enzyme is responsible for the formation of pseudouridine from uracil-516 in 16S ribosomal RNA.
- Escherichia coli hypothetical protein yciL and HI1199, the corresponding Haemophilus influenzae protein.
- Escherichia coli hypothetical protein yjbc.
- Escherichia coli hypothetical protein ymfC and HI0694, the corresponding Haemophilus influenzae protein.
- Aquifex aeolicus hypothetical protein AQ\_554.
- Aquifex aeolicus hypothetical protein AQ\_1464.
- Bacillus subtilis hypothetical protein ypuL.
- Bacillus subtilis hypothetical protein ytzF.
- Borrelia burgdorferi hypothetical protein BB0129.
- Helicobacter pylori hypothetical protein HP1459.
- Synechocystis strain PCC 6803 hypothetical protein slr0361.
- Synechocystis strain PCC 6803 hypothetical protein slr0612.

These are proteins of from 25 to 40 Kd which contain a number of conserved regions in their central section. They can be picked up in the database by the following highly conserved pattern.

- Consensus pattern: G-R-L-D-x(2)-[STA]-x-G-[LIVFA]-[LIVMF](3)-[ST]-[DNST]
- Sequences known to belong to this class detected by the pattern: ALL.
- Other sequence(s) detected in SWISS-PROT: NONE.
- Last update: July 1999 / Pattern and text revised.

[ 1] Wrzesinski J., Bakin A., Nurse K., Lane B.G., Ofengand J.  
Biochemistry 34:8904-8913(1995).

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{END}

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## PROSITE: PS01149

```
ID  PSI_RSU; PATTERN.
AC  PS01149;
DT  NOV-1995 (CREATED); JUL-1999 (DATA UPDATE); JUL-1999 (INFO UPDATE).
DE  Rsu family of pseudouridine synthase signature.
PA  G-R-L-D-x(2) - [STA] -x-G- [LIVFA] - [LIVMF] (3) - [ST] - [DNST].
NR  /RELEASE=38,80000;
NR  /TOTAL=18(18); /POSITIVE=18(18); /UNKNOWN=0(0); /FALSE_POS=0(0);
NR  /FALSE_NEG=0; /PARTIAL=0;
CC  /TAXO-RANGE=???P?; /MAX-REPEAT=1;
DR  P35159, RLUB_BACSU, T; P33918, RSUA_ECOLI, T; P45124, RSUA_HAEIN, T;
DR  O51155, Y129_BORBU, T; Q55578, Y361_SYNY3, T; O66829, Y554_AQUAE, T;
DR  P72581, Y612_SYNY3, T; P42395, YCIL_BUCAP, T; P37765, YCIL_ECOLI, T;
DR  P45104, YCIL_HAEIN, T; P55986, YB59_HELPY, T; O67444, YE64_AQUAE, T;
DR  P32684, YJBC_ECOLI, T; P75966, YMFC_ECOLI, T; P44827, YMFC_HAEIN, T;
DR  Q05668, YRSU_MYCLE, T; Q33210, YRSU_MYCTU, T; Q32068, YTZF_BACSU, T;
DO  PDOC00885;
//
```

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